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(54) Albumin-based nucleotides, their replication and use, and plasmids for use therein.

(57) The DNA sequence coding for human serum albumin has been isolated and inserted as two fragments into two novel plasmids which can be replicated in *E. coli*. These novel fragments can be joined to provide a unitary DNA sequence which then can be cloned into a suitable host, e.g. *E. coli*, for the expression of human serum albumin (which is used extensively in medical practice in treating shock conditions).

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ALBUMIN-BASED NUCLEOTIDES, THEIR REPLICATION AND USE, AND PLASMIDS FOR USE THEREIN

This invention relates to nucleotides related to human serum albumin (HSA), their replication and use, and plasmids (and host substances) for use therein.

The gene for serum albumin is regulated in development. On the other hand, serum albumin is synthesised in mammals by the adult liver, and its plateau in adulthood. The embryonic liver and yolk sac, on the other hand, produce predominantly α-fetoprotein, but the synthesis decreases drastically after birth. Recently, Law et al determined the complete sequence of mouse α-fetoprotein mRNA, Nature 291 (1981) 201-205. The structure revealed extensive homology to mammalian serum albumin, indicating that the two proteins are encoded in the same gene family. Similar conclusions have been reached from studies on the α-fetoprotein genes of the rat and the mouse; see Jagodzinski et al, Proc. Natl. Acad. Sci. USA, 78 (1981) 3521-3525, and Gorin et al, J. Biol. Chem. 256 (1981) 1954-1959.

The complete nucleotide sequence of human serum mRNA has been determined from recombinant cDNA clones and from a primer-extended cDNA synthesis on the mRNA template. The sequence comprises 2,078 nucleotides, starting upstream of a potential ribosome binding site in the 5'-untranslated region. It contains all the translated codons and extends into the poly(A) at the 3'-terminus. Part of the translated sequence codes for a hydrophobic prepeptide met-lys-trp-val-thr-phe-ile-ser-leu-leu-phe-leu-phe-ser-ser-ala-tyr-ser, followed by a basic propeptide arg-gly-val-phe-arg-arg. These signal peptides are absent from mature serum albumin and, so far, have not been identified in their nascent state in humans. A remaining 1,755 nucleotides of the translated mRNA sequence code for 585 amino acids which are in agreement, with few exceptions, with the published amino acid data for human serum albumin. The mRNA sequence verifies and refines the repeating homology in the triple-domain structure of the serum albumin molecule.

~~DETAILED DESCRIPTION OF THE INVENTION~~

Human serum albumin cDNA is cloned into the PstI site of plasmid pBR322 by the oligo(dG)-oligo(dC) tailing technique. Plasmid DNA was isolated from 97 positive colonies which hybridized to the enriched albumin cDNA probe, and the recombinant plasmid pHA36 was found to contain the largest insert of an albumin cDNA sequence. Its restriction endonuclease map is shown in the drawing, together with a restriction map of the primer-extended plasmid clone pHA206. The latter was obtained in a second transformation experiment after initiating the cDNA synthesis from an internal primer. This primer was a 91 base pairs long DNA fragment, MspI(152)-TaqI(182/3), isolated from pHA36. The two plasmids, pHA36 and pHA206, share 0.15 kb of homologous DNA. Together, they encode the entire sequence for human serum albumin, starting with the CTT codon for leu -10 of the prepeptide and extending into the 3'-untranslated region of poly(A).

Sequence of the Albumin cDNA. The sequence was determined for the most part on both DNA strands to ensure accuracy. All of the restriction sites used to end-label DNA fragments were sequenced across by labeling a neighboring restriction site. The entire nucleotide sequence of the serum albumin mRNA, as determined from the cloned DNA in pHA36, pHA206, and from the primer-extended cDNA at the 5'-terminus of the message, is shown in the following Table 1. The inferred amino acid sequence is also indicated. The mRNA length is 2,078 nucleotides, of which 38 represent the 5'-untranslated region, 54 identify a prepeptide of 18 amino acids, 18 identify a propeptide of 6 amino acids, 1,755 code for the known 585 amino acids of serum albumin, 189 make up the 3'-untranslated region and 24 are the poly(A) sequence. Nucleotides 5 to 15 (-34 to -24) in the 5'-untranslated region (Table 1) are complementary to a 3'-terminal region of eukaryotic 18S RNA [Azad, A.A. and Deacon, N.J. (1980) Nucl. Acids Res. 8, 4365-4376] and thus could represent a ribosome binding site:

(5')...T T^{C}T C T T C T G T.....albumin mRNA

(3')...G A G G A A G G C G U C C m_2^6A m_2^6A.....18S RNA

The translated portion of the mRNA sequence codes for the signal peptide and the main body of the albumin polypeptide chain. The

signal peptide is composed of a hydrophobic prepeptide of 18 amino acids and a basic propeptide of 6 amino acids (Table 1). Since prepeptides are removed from nascent secretory proteins (like albumin) in the endoplasmic reticulum, they are seen only in vitro in heterologous translation systems. As yet, they have not been found within cells [Judah, J.D. and Quinn, P.S. (1977) FEBS 11th Mtg., Copenhagen 50, 21-29; and Strauss, A.W., Donohue, A.M., Bennett, C.D., Rodkey, J.A. and Alberts, A.W. (1977) Proc. Natl. Acad. Sci. USA 74, 1358-1362]. This is the first report of the presence and the sequence of a prepeptide for human serum albumin. As it is with other secretory proteins, the conversion of proalbumin to albumin takes place in the Golgi vesicles, and the enzyme responsible for this cleavage is probably cathepsin B [Judah, J.D. and Quinn, P.S. (1978) Nature 271, 384-385]. This is also a first report on the sequence of the propeptide for normal human serum albumin.

At the 3'-end of the message, the putative polyadenylation signal sequence, AATAAA, is located 164 nucleotides downstream from the amino acid termination codon TAA and 16 nucleotides upstream from the beginning of the poly(A) sequence. Another characteristic sequence located near the polyadenylation site has been identified by Benoist, et al. [Benoist, C., O'Hare, K., Breathnach, R. and Chambon, P. (1980) Nucl. Acids Res. 8, 127-142]; the concensus sequence from several mRNAs was concluded as TTTTCACTGC. A similar sequence, TTTTCTCTGT, is located 19 nucleotides upstream from the AATAAA hexanucleotide in the human albumin mRNA (Table 1).

TABLE 1

```
                                                                -18         p r o               -10
                                                                Met lys trp val tlu phe ile ser leu leu phe leu phe ser
                         GCTTTTCTCTTCTGTCAACCCCACAGCCCTTTGGCACA ATG AAG TGG GTA ACC TTT ATT TCC CTT CTT TTT CTC TTT AGC (30)

            -1  -6   p r o          -1  1                                   10                                      20
ser ala tyr ser arg gly val phe arg arg asp ala his lys ser glu val ala his arg phe lys asp leu gly glu glu asn phe lys
TCC GCT TAT TCC AGC GGT GTG TTT CGT CGA GAT GCA CAC AAG AGT GAG GTT GCT CAT CGG TTT AAA GAT TTG GGA GAA GAA AAT TTC AAA (170)

21                                  30              34                      40                                      50
ala leu val leu ile ala phe ala gln tyr leu gln gln cys pro phe glu asp his val lys leu val asn glu val thr glu phe ala
GCC TTG GTG TTG ATT GCC TTT GCT CAG TAT CTT CAG CAG TGT CCA TTT GAA GAT CAT GTA AAA TTA GTG AAT GAA GTA ACT CAA TTT GCA (260)

51      53                          60      62                              70                  75                  80
lys thr cys val ala asp glu ser ala glu asn cys asp lys ser leu his thr leu phe gly asp lys leu cys thr val ala thr leu
AAA ACA TGT GTT GCT GAT GAG TCA GCT GAA AAT TGT GAC AAA TCA CTT CAT ACC CTT TTT GGA GAC AAA TTA TGC ACA GTT GCA ACT CTT (350)

81                                  90  91                                  100 101                                 110
arg glu thr tyr gly glu met ala asp cys cys ala lys gln glu pro gly arg asn glu cys phe leu gln his lys asp asp asn pro
CGT GAA ACC TAT GGT GAA ATG GCT GAC TGC TGT GCA AAA CAA GAA CCT GGG AGA AAT GAA TGC TTC TTG CAA CAC AAA GAT GAC AAC CCA (440)

111                                 120             124                     130                                     140
asn leu pro arg leu val arg pro glu val asp val met cys thr ala phe his asp asn glu glu thr phe leu lys lys tyr leu try
AAC CTC CCC CGA TTG GTG AGA CCA GAG GTT GAT GTG ATG TGC ACT GCT TTT CAT GAC AAT GAA GAG ACA TTT TTG AAA AAA TAC TTA TAT (330)

141                                 150                                     160                             168 169 170
glu ile ala arg arg his pro tyr phe tyr ala pro glu leu leu phe phe ala lys arg tyr lys ala ala phe thr glu cys cys gln
GAA ATT GCC AGA AGA CAT CCT TAC TTT TAT GCC CCG GAA CTC CTT TTC TTT GCT AAA AGG TAT AAA GCT GCT TTT ACA GAA TGT TGC CAA (620)

171                     177         180                                     190                                     200
ala ala asp lys ala ala cys leu leu pro lys leu asp glu leu arg asp glu gly lys ala ser ser ala lys gln arg leu lys cys
GCT GCT GAT AAA GCT GCC TGC CTG TTG CCA AAG CTC GAT GAA CTT CGG GAT GAA GGG AAG GCT TCG TCT GCC AAA CAG AGA CTC AAG TGT (710)

201                                 210                                     220                                     230
ala ser leu gln lys phe gly glu arg ala phe lys ala trp ala val ala arg leu ser gln arg phe pro lys ala glu phe ala glu
GCC AGT CTC CAA AAA TTT GGA GAA AGA GCT TTC AAA GCA TGG GCA GTA GCT CGC CTG AGC CAG AGA TTT CCC AAA GCT GAG TTT GCA GAA (300)
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231                                240                    245 246                 250       253                                     260
val ser lys leu val thr asp leu thr lys val his thr glu cys cys his gly asp leu leu glu cys ala asp asp arg ala asp leu
GTT TCC AAG TTA GTG ACA GAT CTT ACC AAA GTC CAC ACG GAA TGC TGC CAT GGA GAT CTG CTT GAA TGT GCT GAT GAC AGG GCG GAC CTT (890)

261             265                270                                 278 279 280                                 289 290
ala lys tyr ile cys glu asn gln asp ser ile ser ser lys leu lys glu cys cys glu lys pro leu leu glu lys ser his cys ile
GCC AAG TAT ATC TGT GAA AAT CAA GAT TCG ATC TCC AGT AAA CTG AAG GAA TGC TGT GAA AAA CCT CTG TTG GAA AAA TCC CAC TGC ATT (980)

291                                300                                         310                 316                 320
ala glu val glu asn asp glu met pro ala asp leu pro ser leu ala ala asp phe val glu ser lys asp val cys lys asn tyr ala
GCC GAA GTG GAA AAT GAT GAG ATG CCT GCT GAC TTG CCT TCA TTA GCT GCT GAT TTT GTT GAA AGT AAG GAT GTT TGC AAA AAC TAT GCT (1070)

321                                330                                         340                                     350
glu ala lys asp val phe leu gly met phe leu tyr glu tyr ala arg arg his pro asp tyr ser val val leu leu leu arg leu ala
GAG GCA AAG GAT GTC TTC TTG GGC ATG TTT TTG TAT GAA TAT GCA AGA AGG CAT CCT GAT TAC TCT GTC GTG CTG CTG CTG AGA CTT GCC (1160)

351                                360 361                             369 370                                         380
lys thr tyr glu thr thr leu glu lys cys cys ala ala ala asp pro his glu cys tyr ala lys val phe asp glu phe lys pro leu
AAG ACA TAT GAA ACC ACT CTA GAG AAG TGC TGT GCC GCT GCA GAT CCT CAT GAA TGC TAT GCC AAA GTG TTC GAT GAA TTT AAA CCT CCT (1250)

381                                390     392                                 400                                     410
val glu glu pro gln asn leu ile lys gln asn cys glu leu phe glu gln leu gly glu tyr lys phe gln asn ala leu leu val arg
GTG GAA GAG CCT CAG AAT TTA ATC AAA CAA AAT TGT GAC CTT TTT CAG CAG CTT GGA GAG TAC AAA TTC CAG AAT GCG CTG TTA GTT CGT (1340)

411                                420                                 430                             437 438     440
tyr thr lys lys val pro gln val ser thr pro thr leu val glu val ser arg asn leu gly lys val gly ser lys cys cys lys his
TAC ACC AAG AAA GTA CCC CAA GTG TCA ACT CCA ACT CTT GTA GAG GTC TCA AGA AAC CTA GGA AAA GTG GGC AGC AAA TGT TGT AAA CAT (1430)

441                        448     450                                 460 461                                     470
pro glu ala lys arg met pro cys ala glu asp tyr leu ser val val leu asn gln leu cys val leu his glu lys thr pro val ser
CCT GAA GCA AAA AGA ATG CCC TGT GCA GAA GAC TAT CTA TCC GTG GTC CTG AAC CAG TTA TGT GTG TTG CAT GAG AAA ACG CCA GTA AGT (1520)

471                 476 477        480                                 490                                     500
asp arg val thr lys cys cys thr glu ser leu val asn arg arg pro cys phe ser ala leu glu val asp glu thr tyr val pro lys
GAC AGA GTC ACC AAA TGC TGC ACA GAA TCC TTG GTG AAC AGG CGA CCA TGC TTT TCA GCT CTG GAA GTC GAT GAA ACA TAC GTT CCC AAA (1610)

501                                510         514                     520                                     530
glu phe asn ala glu thr phe thr phe his ala asp ile cys thr leu ser glu lys glu arg gln ile lys lys gln thr ala leu val
GAG TTT AAT GCT GAA ACA TTC ACC TTC CAT GCA GAT ATA TGC ACA CTT TCT GAG AAG GAG AGA CAA ATC AAG AAA CAA ACT GCA CTT GTT (1700)
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                                                                  558 559 560
531                 540                 550
glu leu val lys his lys pro lys ala thr lys glu gln leu lys ala val met asp phe ala ala phe val glu lys cys cys lys
GAG CTC GTG AAA CAC AAG CCC AAG GCA ACA AAA GAG CAA CTG AAA GCT GTT ATG GAT GAT TTC GCT GCT TTT GTA GAG AAG TGC TGT AAG (1790)

561                 567         570                 580
ala asp asp lys glu thr cys phe ala glu glu gly lys lys leu val ala ala ser gln ala ala leu gly leu ter          ter
GCT GAC GAT AAG GAG ACC TGC TTT GCC GAG GAG GGT AAA AAA CTT GTT GCT GCA AGT CAA GCT GCC TTA GGC TTA TAA CATCACATTTAAAAG (1883)

      ter  ter
CATCTCAGCCTACCATGAGAATAAGAGAAAGAAAATGAAGATCAAAAGCTTATTCATCTGTTTTTCTTTTTCGTTGGTGTAAAGCCAACACCCTGTCTAAAAAACATAAATTTCTTTAA (2002)

TCATTTTGCCTCTTTTCTCTGTGCTTCAATTAATAAAAATGGAAAGAATCTAA..... 20 .....AA (2078)
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Following are examples which illustrate procedures~~, including the best mode,~~ for practicing the invention. These examples should not be construed as limiting. All percentages are by weight and all solvent mixture proportions are by volume unless otherwise noted.

Example 1 Isolation of Messenger RNA

Human liver mRNA was obtained following the procedure of Chirgwin, et al [Chirgwin, J.M., Przybyla, A.E., MacDonald, R.J. and Rutter, W.J. (1979) Biochemistry 18, 5294-5299]. Immunoprecipitation of albumin containing polysomes was performed according to Taylor and Tse [Taylor, J.M. and Tse, T.P.H. (1976) J. Biol. Chem. 251, 7461-7467]. In vitro translation of mRNA was carried out in a reticulocyte cell-free system, following the instruction of the manufacturer (New England Nuclear). The translation products were separated electrophoretically according to Laemmli [Laemmli, J.K. (1970) Nature 227, 680-685.

Example 2 Cloning Procedures

Double stranded cDNA was synthesized as described previously [Law, S., Tamaoki, T., Kreuzaler, F. and Dugaiczyk, A. (1980) Gene 10, 53-61]. It was annealed to PstI-linearized pBR322 DNA [Rolivar, F., Rodriguez, R.L., Greene, P.J., Betlach, M.C., Heyneker, H.L., Boyer, H.W., Crossa, J.H. and Falkow, S. (1977) Gene 2, 95-113] that had been tailed with 15 dG residues/3'-terminus [Dugaiczyk, A., Robberson, D.L. and Ullrich, A. (1980) Biochemistry 19, 5869-5873]. The annealed DNA was used to transform E. coli strain RR1, as detailed previously [Law, S., et al., Ibid.]. The albumin clones were selected using the colony hybridization method of Grunstein and Hogness [Grunstein, M. and Hogness, D.S. (1975) Proc. Natl. Acad. Sci. USA 72, 3961-3965], with [^{32}P]-labeled cDNA synthesized with the immunoprecipitated polysomal mRNA as template.

As shown in Example 5, plasmids pHA36 and pHA206 were deposited in E. coli HB101 hosts. The plasmids were obtained from E. coli RR1 hosts, described in this example, and transformed into E. coli HB101 by standard procedures well known to those of ordinary skill in this art. The E. coli RR1 hosts were lysed and then centrifuged to separate the chromosomal DNA, cell DNA and plasmid DNA. The plasmid DNA, remaining in the supernatant, is precipitated with ethanol and the precipitate is resuspended in buffer, e.g., TCM (10mM Tris·HCl, pH 8.0, 10 mM $CaCl_2$, 10 mM $MgCl_2$). The cells for transformation are

prepared as follows: 120 ml of L-broth (1% tryptone, 0.5% yeast extract, 0.5% NaCl) are inoculated with an 18 hour culture of HB101 NRRL B-11371 and grown to an optical density of 0.6 at 600 nm. Cells are washed in cold 100 mM NaCl and resuspended for 15 minutes in 20 ml chilled 50 mM $CaCl_2$. Bacteria are then concentrated to one-tenth of this volume in $CaCl_2$ and mixed 2:1 (v:v) with annealed plasmid DNA, prepared as described above. After chilling the cell-DNA mixture for 15 minutes, it is heat shocked at 42°C for 2 minutes, then allowed to equilibrate at room temperature for ten minutes before addition of L-broth 10 times the volume of the cell-DNA suspension. Transformed cells are incubated in broth at 37°C for one hour before inoculating selective media (L-agar plus 10 µg/ml tetracycline) with 200 µl/plate. Plates are incubated at 37°C for 48 hours to allow the growth of transformants.

Example 3 Mapping of Restriction Endonuclease Sites

Restriction endonucleases were obtained from Bethesda Research Laboratories and New England Biolabs and were used according to the manufacturers' instructions. The digested DNA fragments were analyzed electrophoretically on agarose [Helling, R.B., Goodman, H.M. and Boyer, H.W. (1974) J. Virol. 14, 1235-1244] or acrylamide [Dingman, C., Fisher, M.P. and Kakefuda, T. (1972) Biochemistry 11, 1242-1250] gels.

Example 4 DNA Sequencing

DNA fragments were dephosphorylated with bacterial alkaline phosphatase (Worthington) and labeled at the 5'-ends with polynucleotide kinase (Boehringer-Mannheim) and $\gamma[^{32}P]$ATP. Following digestion with a second restriction endonuclease and electrophoretic separation of the fragments, DNA sequence determination was done according to the procedure of Maxam and Gilbert [Maxam, A. and Gilbert, W. (1980) Methods Enzym. 65, 499-560] and the degradation products were separated electrophoretically on 0.4 mm acrylamide gels as described by Sanger and Coulson [Sanger, F. and Coulson, R. (1978) FEBS Letters 87, 107-110].

Example 5 Recombinant Plasmids pHA36 and pHA206

As disclosed in Example 2, albumin clones were selected by hybridizing to the enriched albumin cDNA probe. Plasmid pHA36 contained the largest insert of an albumin cDNA sequence. Both plasmids pHA36 and pHA206 have been deposited in a viable E. coli host in the

permanent collection of the Northern Regional Research Laboratory (NRRL), U.S. Department of Agriculture, Peoria, Illinois, U.S.A. Their accession numbers in this repository are as follows:

HB101(pHA36) - NRRL B-12551

HB101(pHA206) - NRRL B-12550

E. coli HB101 is a known and widely available host microbe. Its NRRL accession number is NRRL B-11371.

NRRL B-12550 and NRRL B-12551 are available to the public. ~~upon the grant of a patent. It should be understood that the availability~~ of these deposits does not constitute a license to practice the subject invention in derogation of patent rights granted with the subject ~~instrument by governmental action.~~

E. coli RR1 and E. coli HB101 are known and widely available host microbes. Their NRRL accession numbers are NRRL B-12186 and NRRL B-11371, respectively.

pBR322 is a well known and widely available plasmid. It can be obtained from the following host deposit by standard procedures:

NRRL B-12014 - E. coli RR1 (pBR322).

YEp6 is a well known and widely available yeast episomal plasmid. It can be obtained from the following host deposit by standard procedures:

E. coli HB101 (YEp6) - NRRL B-12093.

Example 6 Assembly of the Serum Albumin Gene

Assembling the pieces together is a straighforward task of restriction enzymology. There is only one MspI site in the overlapping DNA sequence of the two cDNA clones. Two enzymatic steps of (i) MspI digestion of the two DNAs, followed by (ii) the use of ligase, an enzyme that seals DNA fragments, will give the desired product. Although two other undesired DNA species will also be obtained in the course of this recombination reaction, both of them will differ substantially in size. Thus, separation and isolation of the desired DNA species will be achieved.

The assembled DNA clone can be used to transform two types of cells:

(a) Escherichia coli

(b) Saccharomyces cerevisiae

(a) The vector of choice is plasmid pBR322, the same that has

been successfully used for cloning of the two fragmented pieces of the serum albumin cDNA.

(b) In order to transform yeast with the serum albumin structural gene sequence, the DNA must be inserted into one of the existing yeast plasmid vectors. This can be accomplished by taking advantage of the fact that several restriction endonuclease recognition sequences are absent from the cloned serum albumin DNA. Synthetic EcoR1 DNA linkers can be ligated to the DNA fragment containing the serum albumin sequence followed by insertion (ligation) into one of the yeast plasmid vectors, e.g., YEp6, at the Eco R1 cloning site. The fused chimeric plasmid can be used to transform yeast according to an established procedure [Hinnen, A., Hicks, J.B. and Fink, G.R. (1978) Proc. Natl. Acad. Sci. USA, 75, 1929]. YEp6 can be obtained from the NRRL repository, as disclosed supra.

Example 7 Expression of the Serum Albumin Gene

The main body of the structural gene will be transcribed by the E. coli or yeast enzymes. If little or no albumin is produced with the selected host, then an Escherichia coli promoter DNA sequence carrying an initiation codon, i.e., ATG, can be ligated at the beginning of the serum albumin structural gene. Such elements are known and available, e.g., lac promoter used for the expression of human interferon gene in E. coli [Proc. Natl. Acad. Sci. 77, 5230 (1980)]; source of promoter DNA [Proc. Natl. Acad. Sci. 76, 760 (1979)]. Also, see Nature, Vol. 281, October 18, 1979. It has already been documented that such Escherichia coli promoter sequences function well in the expression of foreign genes in Escherichia coli [Mercereau-Puijalon, O., Royal, A., Cami, B., Garapin, A., Krust, A., Gannon, I. and Kourilsky, P. (1978) Nature 275, 505; and Goeddel, D.V., Kleid, D.G., Bolivar, F., Heyneker, H.L., Yansura, D.G., Grea, R., Hirose, T., Kraszewski, A., Itakura, K., and Riggs, A. (1979) Natl. Acad. Sci. USA 76, 106]. For expression in yeast, see Rose, M., Casadaban, M.J. and Botstein, D. (1981) Proc. Natl. Acad. Sci. USA 78, 2460 and 4466.

Example 8 Screening of Clones Producing Albumin

Immunological methods can be used to detect small amounts of albumin made in a bacterium. Flat disks of flexible polyvinyl are coated with the IgG fraction from an immune serum and the disks are pressed onto an agar plate so that antigen released from an in situ lysed microbial colony can bind to the fixed antibody. The plastic

disk is then incubated with the same total IgG fraction labeled with radioactive iodine so that other determinants on the bound antigen can in turn bind the iodinated antibody. Radioactive areas on the disk expose X-ray film during autoradiography and thus identify colonies producing the protein which is being screened for. Detailed protocols of this procedure have been published [Broome, S. and Gilbert, W. (1978) Proc. Natl. Acad. Sci. USA, 75, 2746]. The purification of human serum albumin can be accomplished by using procedures well known in the art. For example, procedures disclosed in a chapter by T. Peters: Purification and Properties of Serum Albumin, in: The Plasma Proteins, Putnam, Ed. Academic Press, New York, 1975, can be used.

The work described herein was all done in conformity with physical and biological containment requirements specified in the NIH Guidelines.

CLAIMS

1. Plasmid pHA36, having a restriction endonuclease pattern as shown in the drawing.

2. Plasmid pHA206, having a restriction endonuclease pattern as shown in the drawing.

3. E. coli HB101 (pHA36) having the deposit accession number NRRL B-12551.

4. E. coli HB101 (pHA206) having the deposit accession number NRRL B-12550.

5. A microorganism modified to contain a nucleotide sequence coding for the amino acid sequence of human serum albumin; said nucleotide sequence is as follows:

```
35              30              25              20              15              10               5
                                                                                -10
                                                                                  leu phe leu phe ser
                                                                                  CTT TTT CTC TTT AGC  (30)

          -1  -6    p r o    -1  1                              10                                  20
ser ala tyr ser arg gly val phe arg arg asp ala his lys ser glu val ala his arg phe lys asp leu gly glu glu asn phe lys
TCG GCT TAT TCC AGG GGT GTG TTT CGT CGA GAT GCA CAC AAG AGT GAG GTT GCT CAT CGG TTT AAA GAT TTG GGA GAA GAA AAT TTC AAA (170)

 21                             30            34                  40                                  50
ala leu val leu ile ala phe ala gln tyr leu gln gln cys pro phe glu asp his val lys leu val asn glu val thr glu phe ala
GCC TTG GTG TTG ATT GCC TTT GCT CAG TAT CTT CAG CAG TGT CCA TTT GAA GAT CAT GTA AAA TTA GTG AAT GAA GTA ACT CAA TTT GCA (260)

 51      53                     60      62                  70              75                  80
lys thr cys val ala asp glu ser ala glu asn cys asp lys ser leu his thr leu phe gly asp lys leu cys thr val ala thr leu
AAA ACA TGT GTT GCT GAT GAG TCA GCT GAA AAT TGT GAC AAA TCA CTT CAT ACC CTT TTT GGA GAC AAA TTA TGC ACA GTT GCA ACT CTT (350)

 81                             90  91                  100 101                                 110
arg glu thr tyr gly glu met ala asp cys cys ala lys gln glu pro gly arg asn glu cys phe leu gln his lys asp asp asn pro
CGT GAA ACC TAT GGT GAA ATG GCT GAC TGC TGT GCA AAA CAA GAA CCT GGG AGA AAT GAA TGC TTC TTG CAA CAC AAA GAT GAC AAC CCA (440)

111                             120           124                 130                                 140
asn leu pro arg leu val arg pro glu val asp val met cys thr ala phe his asp asn glu glu thr phe leu lys lys tyr leu try
AAC CTC CCC CGA TTG GTG AGA CCA GAG GTT GAT GTG ATG TGC ACT GCT TTT CAT GAC AAT GAA GAG ACA TTT TTG AAA AAA TAC TTA TAT (530)

141                             150                 160                             168 169 170
glu ile ala arg arg his pro tyr phe tyr ala pro glu leu leu phe phe ala lys arg tyr lys ala ala phe thr glu cys cys gln
GAA ATT GCC AGA AGA CAT CCT TAC TTT TAT GCC CCG GAA CTC CTT TTC TTT GCT AAA AGG TAT AAA GCT GCT TTT ACA GAA TGT TGC CAA (620)

171                     177     180                 190                                 200
ala ala asp lys ala ala cys leu leu pro lys leu asp glu leu arg asp glu gly lys ala ser ser ala lys gln arg leu lys cys
GCT GCT GAT AAA GCT GCC TGC CTG TTG CCA AAG CTC GAT GAA CTT CGG GAT GAA GGG AAG GCT TCG TCT GCC AAA CAG AGA CTC AAG TGT (710)

201                             210                 220                                 230
ala ser leu gln lys phe gly glu arg ala phe lys ala trp ala val ala arg leu ser gln arg phe pro lys ala glu phe ala glu
GCC AGT CTC CAA AAA TTT GGA GAA AGA GCT TTC AAA GCA TGG GCA GTA GCT CGC CTG AGC CAG AGA TTT CCC AAA GCT GAG TTT GCA GAA (800)
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231                                 240                 245 246             250         253                         260
val ser lys leu val thr asp leu thr lys val his thr glu cys cys his gly asp leu leu glu cys ala asp asp arg ala asp leu
GTT TCC AAG TTA GTG ACA GAT CTT ACC AAA GTC CAC ACG GAA TGC TGC CAT GGA GAT CTG CTT GAA TGT GCT GAT GAC AGG GCG GAC CTT (890)

261             265                 270                             278 279 280                             289 290
ala lys tyr ile cys glu asn gln asp ser ile ser ser lys leu lys glu cys cys glu lys pro leu leu glu lys ser his cys ile
GCC AAG TAT ATC TGT GAA AAT CAA GAT TCG ATC TCC AGT AAA CTG AAG GAA TGC TGT GAA AAA CCT CTG TTG GAA AAA TCC CAC TGC ATT (980)

291                                 300                                 310                 316             320
ala glu val glu asn asp glu met pro ala asp leu pro ser leu ala ala asp phe val glu ser lys asp val cys lys asn tyr ala
GCC GAA GTG GAA AAT GAT GAG ATG CCT GCT GAC TTG CCT TCA TTA GCT GCT GAT TTT GTT GAA AGT AAG GAT GTT TGC AAA AAC TAT GCT (1070)

321                                 330                                 340                             350
glu ala lys asp val phe leu gly met phe leu tyr glu tyr ala arg arg his pro asp tyr ser val val leu leu leu arg leu ala
GAG GCA AAG GAT GTC TTC TTG GGC ATG TTT TTG TAT GAA TAT GCA AGA AGG CAT CCT GAT TAC TCT GTC GTG CTG CTG CTG AGA CTT GCC (1160)

351                                 360 361                             369 370                             380
lys thr tyr glu thr thr leu glu lys cys cys ala ala ala asp pro his glu cys tyr ala lys val phe asp glu phe lys pro leu
AAG ACA TAT GAA ACC ACT CTA GAG AAG TGC TGT GCC GCT GCA GAT CCT CAT GAA TGC TAT GCC AAA GTG TTC GAT GAA TTT AAA CCT CCT (1250)

381                                 390     392                         400                             410
val glu glu pro gln asn leu ile lys gln asn cys glu leu phe glu gln leu gly glu tyr lys phe gln asn ala leu leu val arg
GTG GAA GAG CCT CAG AAT TTA ATC AAA CAA AAT TGT GAG CTT TTT GAG CAG CTT GGA GAG TAC AAA TTC CAG AAT GCG CTG TTA GTT CGT (1340)

411                                 420                                 430                 437 438     440
tyr thr lys lys val pro gln val ser thr pro thr leu val glu val ser arg asn leu gly lys val gly ser lys cys cys lys his
TAC ACC AAG AAA GTA CCC CAA GTG TCA ACT CCA ACT CTT GTA GAG GTC TCA AGA AAC CTA GGA AAA GTG GGC AGC AAA TGT TGT AAA CAT (1430)

441                         448     450                                 460 461                             470
pro glu ala lys arg met pro cys ala glu asp tyr leu ser val val leu asn gln leu cys val leu his glu lys thr pro val ser
CCT GAA GCA AAA AGA ATG CCC TGT GCA GAA GAC TAT CTA TCC GTG GTC CTG AAC CAG TTA TGT GTG TTG CAT GAG AAA ACG CCA GTA AGT (1520)

471                 476 477         480                             490                             500
asp arg val thr lys cys cys thr glu ser leu val asn arg arg pro cys phe ser ala leu glu val asp glu thr tyr val pro lys
GAC AGA GTC ACC AAA TGC TGC ACA GAA TCC TTG GTG AAC AGG CGA CCA TGC TTT TCA GCT CTG GAA GTC GAT GAA ACA TAC GTT CCC AAA (1610)

501                                 510             514                 520                             530
glu phe asn ala glu thr phe thr phe his ala asp ile cys thr leu ser glu lys glu arg gln ile lys lys gln thr ala leu val
GAG TTT AAT GCT GAA ACA TTC ACC TTC CAT GCA GAT ATA TGC ACA CTT TCT GAG AAG GAG AGA CAA ATC AAG AAA CAA ACT GCA CTT GTT (1700)
```

```
                                                                    558 559 560
531                 540                 550
glu leu val lys his lys pro lys ala thr lys glu gln leu lys ala val met asp asp phe ala ala phe val glu lys cys cys lys
GAG CTC GTG AAA CAC AAG CCC AAG GCA ACA AAA GAG CAA CTG AAA GCT GTT ATG GAT GAT TTC GCT TTT GTA GAG AAG TGC TGC AAG (1790)

561                 567         570                 580
ala asp asp lys glu thr cys phe ala glu glu gly lys lys leu val ala ala ser gln ala ala leu gly leu ter          ter
GCT GAC GAT AAG GAG ACC TGC TTT GCC GAG GAG GGT AAA AAA CTT GTT GCT GCA AGT CAA GCT GCC TTA GGC TTA TAA CATCACATTTAAAAG (1883)

      ter   ter
CATCTCACGCCTACCATGAGAATAAGAGAAAGAAATGAACATCAAAAGCTTATTCATCTGTTTTTCTTTTTCGTTGGTGTAAAGCCAACACCCTGTCTAAAAAACATAAATTTCTTTTAA (2002)

TCATTTTGCCTCTTTTCTCTGTGCTTCAATTAATAAAAAATGGAAAGAATCTAA..... 20 .....AA (2078)
```

6. Nucleotide sequence of the cDNA of human serum albumin, said nucleotide sequence is as follows:

```
                                                                  10                  20
                1                                                 |                   |
                asp ala his lys ser glu val ala his arg phe lys asp leu gly glu glu asn phe lys
                GAT GCA CAC AAG AGT GAG GTT GCT CAT CGC TTT AAA GAT TTG GGA GAA GAA AAT TTC AAA (170)

                                                                  40                  50
           21                   30                  34            |                   |
           ala leu val leu ile ala phe ala gln tyr leu gln gln cys pro phe glu asp his val lys leu val asn glu val thr glu phe ala
           GCC TTG GTG TTG ATT GCC TTT GCT CAG TAT CTT CAG CAG TGT CCA TTT GAA GAT CAT GTA AAA TTA GTG AAT GAA GTA ACT GAA TTT GCA (260)

                                                                  70                  80
           51                   53                  62            |                   |
           lys thr cys val ala asp glu ser ala glu asn cys asp lys ser leu his thr leu phe gly asp lys leu cys thr val ala thr leu
           AAA ACA TGT GTT GCT GAT GAG TCA GCT GAA AAT TGT GAC AAA TCA CTT CAT ACC CTT TTT CGA GAC AAA TTA TGC ACA GTT GCA ACT CTT (350)

                                                                  100 101             110
           81                   90  91                           |   |               |
           arg glu thr tyr gly glu met ala asp cys cys ala lys gln glu pro gly arg asn glu cys phe leu gln his lys asp asp asn pro
           CGT GAA ACC TAT GGT GAA ATG GCT GAC TGC TGT GCA AAA CAA GAA CCT GGG AGA AAT GAA TGC TTC TTG CAA CAC AAA GAT GAC AAC CCA (440)

                                                                  130                 140
           111                  120                 124           |                   |
           asn leu pro arg leu val arg pro glu val asp val met cys thr ala phe his asp asn glu glu thr phe leu lys lys tyr leu try
           AAC CTC CCC CGA TTG GTG AGA CCA GAG GTT GAT GTG ATG TGC ACT GCT TTT CAT GAC AAT GAA GAG ACA TTT TTG AAA AAA TAC TTA TAT (530)

                                                                  160                 168 169 170
           141                  150                             |                   |   |   |
           glu ile ala arg arg his pro tyr phe tyr ala pro glu leu leu phe phe ala lys arg tyr lys ala ala phe thr glu cys cys gln
           GAA ATT GCC AGA AGA CAT CCT TAC TTT TAT GCC CCG GAA CTC CTT TTC TTT GCT AAA AGG TAT AAA GCT GCT TTT ACA GAA TGT TGC CAA (620)

                                                                  190                 200
           171                  177         180                  |                   |
           ala ala asp lys ala ala cys leu pro lys leu asp glu leu arg asp glu gly lys ala ser ser ala lys gln arg leu lys cys
           GCT GCT GAT AAA GCT GCC TGC CTG TTG CCA AAG CTC GAT GAA CTT CGG GAT GAA GGG AAG GCT TCG TCT GCC AAA CAG AGA CTC AAG TGT (710)

                                                                  220                 230
           201                  210                             |                   |
           ala ser leu gln lys phe gly glu arg ala phe lys ala trp ala val ala arg leu ser gln arg phe pro lys ala glu phe ala glu
           GCC AGT CTC CAA AAA TTT GGA GAA AGA GCT TTC AAA GCA TGG GCA GTA GCT CGC CTG AGC CAG AGA TTT CCC AAA GCT GAG TTT GCA GAA (800)
```

```
231                                240                245 246         250     253                         260
val ser lys leu val thr asp leu thr lys val his thr glu cys cys his gly asp leu leu glu cys ala asp asp arg ala asp leu
GTT TCC AAG TTA GTG ACA GAT CTT ACC AAA GTC CAC ACG GAA TGC TGC CAT GGA GAT CTG CTT GAA TGT GCT GAT GAC AGG GCG GAC CTT (890)

261             265                270                            278 279 280                               289 290
ala lys tyr ile cys glu asn gln asp ser ile ser ser lys leu lys glu cys cys glu lys pro leu leu glu lys ser his cys ile
GCC AAG TAT ATC TGT GAA AAT CAA GAT TCG ATC TCC AGT AAA CTG AAG GAA TGC TGT GAA AAA CCT CTG TTG GAA AAA TCC CAC TGC ATT (980)

291                                300                                    310                     316         320
ala glu val glu asn asp glu met pro ala asp leu pro ser leu ala ala asp phe val glu ser lys asp val cys lys asn tyr ala
GCC GAA GTG GAA AAT GAT GAG ATG CCT GCT GAC TTG CCT TCA TTA GCT GCT GAT TTT GTT GAA AGT AAG GAT GTT TGC AAA AAC TAT GCT (1070)

321                                330                                    340                                 350
glu ala lys asp val phe leu gly met phe leu tyr glu tyr ala arg arg his pro asp tyr ser val val leu leu leu arg leu ala
GAG GCA AAG GAT GTC TTC TTG GGC ATG TTT TTG TAT GAA TAT GCA AGA AGG CAT CCT GAT TAC TCT GTC GTG CTG CTG CTG AGA CTT GCC (1160)

351                                360 361                        369 370                                     380
lys thr tyr glu thr thr leu glu lys cys cys ala ala ala asp pro his glu cys tyr ala lys val phe asp glu phe lys pro leu
AAG ACA TAT GAA ACC ACT CTA GAG AAG TGC TGT GCC GCT GCA GAT CCT CAT GAA TGC TAT GCC AAA GTG TTC GAT GAA TTT AAA CCT CCT (1250)

381                                390 392                                400                                     410
val glu glu pro gln asn leu ile lys gln asn cys glu leu phe glu gln leu gly glu tyr lys phe gln asn ala leu leu val arg
GTG GAA GAG CCT CAG AAT TTA ATC AAA CAA AAT TGT GAG CTT TTT GAG CAG CTT GGA GAG TAC AAA TTC CAG AAT GCG CTG TTA GTT CGT (1340)

411                                420                                    430                         437 438   440
tyr thr lys lys val pro gln val ser thr pro thr leu val glu val ser arg asn leu gly lys val gly ser lys cys cys lys his
TAC ACC AAG AAA GTA CCC CAA GTG TCA ACT CCA ACT CTT GTA GAG GTC TCA AGA AAC CTA GGA AAA GTG GGC AGC AAA TGT TGT AAA CAT (1430)

441                        448     450                                    460 461                             470
pro glu ala lys arg met pro cys ala glu asp tyr leu ser val val leu asn gln leu cys val leu his glu lys thr pro val ser
CCT GAA GCA AAA AGA ATG CCC TGT GCA GAA GAC TAT CTA TCC GTG GTC CTG AAC CAG TTA TGT GTG TTG CAT GAG AAA ACG CCA GTA AGT (1520)

471             476 477        480                                    490                                     500
asp arg val thr lys cys cys thr glu ser leu val asn arg arg pro cys phe ser ala leu glu val asp glu thr tyr val pro lys
GAC AGA GTC ACC AAA TGC TGC ACA GAA TCC TTG GTG AAC AGG CGA CCA TGC TTT TCA GCT CTG GAA GTC GAT GAA ACA TAC GTT CCC AAA (1610)

501                                510             514                520                                     530
glu phe asn ala glu thr phe thr phe his ala asp ile cys thr leu ser glu lys glu arg gln ile lys lys gln thr ala leu val
GAG TTT AAT GCT GAA ACA TTC ACC TTC CAT GCA GAT ATA TGC ACA CTT TCT GAG AAG GAG AGA CAA ATC AAG AAA CAA ACT GCA CTT GTT (1700)
```

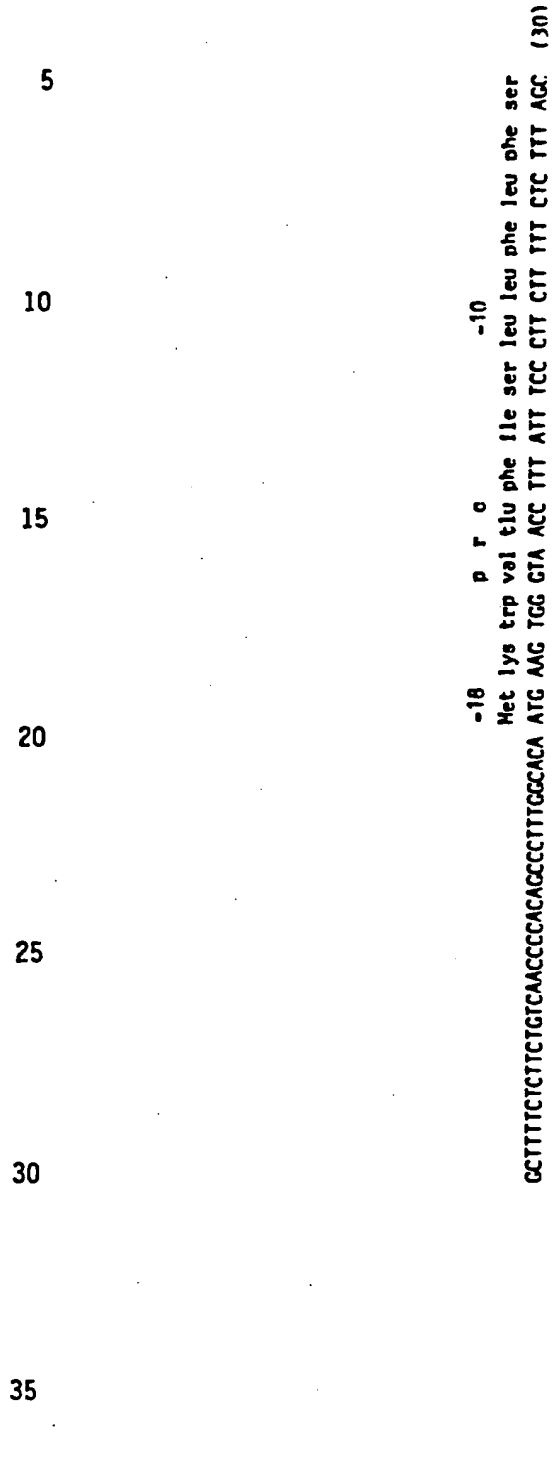
```
                                                                  558 559 560
531                                          550
glu leu val lys his lys pro lys ala thr lys glu gln leu lys ala val met asp asp phe ala ala phe val glu lys cys cys lys
GAG CTC GTG AAA CAC AAG CCC AAG GCA ACA AAA GAG CAA CTC AAA GCT GTT ATG GAT GAT TTC GCT GCT TTT GTA GAG AAG TGC TGC AAG (1790)

                                  567                 580
561                      570
ala asp asp lys glu thr cys phe ala glu glu gly lys lys leu val ala ala ser gln ala ala leu gly leu ter          ter
GCT GAC GAT AAG GAG ACC TGC TTT GCC GAG GAC GGT AAA AAA CTT GTT GCT GCA AGT CAA GCT GCC TTA GGC TTA TAA CATCACATTTAAAAG (1883)

          ter   ter
CATCTCAGCCTACCATGAGAATAAGAGAAAGAAAATGAAGATCAAAAGCTTATTCATCTGTTTTTTCTTTTTCGTTGGTGTAAAGCCAACACCCTGTCTAAAAAACATAAATTTCTTTAA (2002)

TCATTTTGCCTCTTTTCTCTGTGCTTCAATTAATAAAAAATGGAAAGAATCTAA..... 20 .....AA (2078)
```

7. Nucleotide sequence coding for the prepeptide of human serum albumin, said nucleotide sequence is as follows:



8. Nucleotide sequence coding for pro human serum albumin, said nucleotide sequence is as follows:

```
                         -6   p   r   o  -1   1                                  10                                          20
                        arg gly val phe arg arg asp ala his lys ser glu val ala his arg phe lys asp leu gly glu glu asn phe lys
                        AGG GGT GTG TTT CGT CGA GAT GCA CAC AAG AGT GAG GTT GCT CAT CGG TTT AAA GAT TTG GGA GAA GAA AAT TTC AAA (170)

21                                      30      34                              40                                          50
ala leu val leu ile ala phe ala gln tyr leu gln gln cys pro phe glu asp his val lys leu val asn glu val thr glu phe ala
GCC TTG GTG TTG ATT GCC TTT GCT CAG TAT CTT CAG CAG TGT CCA TTT GAA GAT CAT GTA AAA TTA GTG AAT GAA GTA ACT GAA TTT GCA (260)

51      53                              60      62                              70                  75                  80
lys thr cys val ala asp glu ser ala glu asn cys asp lys ser leu his thr leu phe gly asp lys leu cys thr val ala thr leu
AAA ACA TGT GTT GCT GAT GAG TCA GCT GAA AAT TGT GAC AAA TCA CTT CAT ACC CTT TTT GGA GAC AAA TTA TGC ACA GTT GCA ACT CTT (350)

81                                      90  91                              100 101                                     110
arg glu thr tyr gly glu met ala asp cys cys ala lys gln glu pro gly arg asn glu cys phe leu gln his lys asp asp asn pro
CGT GAA ACC TAT GGT GAA ATG GCT GAC TGC TGT GCA AAA CAA GAA CCT GGG AGA AAT GAA TGC TTC TTG CAA CAC AAA GAT GAC AAC CCA (440)

111                                     120         124                         130                                     140
asn leu pro arg leu val arg pro glu val asp val met cys thr ala phe his asp asn glu glu thr phe leu lys lys tyr leu try
AAC CTC CCC CGA TTG GTG AGA CCA GAG GTT GAT GTG ATG TGC ACT GCT TTT CAT GAC AAT GAA GAG ACA TTT TTG AAA AAA TAC TTA TAT (330)

141                                     150                                     160                         168 169 170
glu ile ala arg arg his pro tyr phe tyr ala pro glu leu leu phe phe ala lys arg tyr lys ala ala phe thr glu cys cys gln
GAA ATT GCC AGA AGA CAT CCT TAC TTT TAT GCC CCG GAA CTC CTT TTC TTT GCT AAA AGG TAT AAA GCT GCT TTT ACA GAA TGT TGC CAA (620)

171                         177         180                                     190                                     200
ala ala asp lys ala ala cys leu leu pro lys leu asp glu leu arg asp glu gly lys ala ser ser ala lys gln arg leu lys cys
GCT GCT GAT AAA GCT GCC TGC CTG TTG CCA AAG CTC GAT GAA CTT CGG GAT GAA GGG AAG GCT TCG TCT GCC AAA CAG AGA CTC AAG TGT (710)

201                                     210                                     220                                     230
ala ser leu gln lys phe gly glu arg ala phe lys ala trp ala val ala arg leu ser gln arg phe pro lys ala glu phe ala glu
GCC AGT CTC CAA AAA TTT GGA GAA AGA GCT TTC AAA GCA TGG GCA GTA GCT CGC CTG AGC CAG AGA TTT CCC AAA GCT GAG TTT GCA GAA (300)
```

```
231                                      240                   245 246          250          253                      260
val ser lys leu val thr asp leu thr lys val his thr glu cys cys his gly asp leu leu glu cys ala asp asp arg ala asp leu
GTT TCC AAG TTA GTG ACA GAT CTT ACC AAA GTC CAC ACG GAA TGC TGC CAT GGA GAT CTG CTT GAA TGT GCT GAT GAC AGG GCG GAC CTT (890)

261             265                      270                                   278 279 280                        289 290
ala lys tyr ile cys glu asn gln asp ser ile ser ser lys leu lys glu cys cys glu lys pro leu leu glu lys ser his cys ile
GCC AAG TAT ATC TGT GAA AAT CAA GAT TCG ATC TCC AGT AAA CTG AAG GAA TGC TGT GAA AAA CCT CTG TTG GAA AAA TCC CAC TGC ATT (980)

291                                      300                                           310             316            320
ala glu val glu asn asp glu met pro ala asp leu pro ser leu ala ala asp phe val glu ser lys asp val cys lys asn tyr ala
GCC GAA GTG GAA AAT GAT GAG ATG CCT GCT GAC TTG CCT TCA TTA GCT GCT GAT TTT GTT GAA AGT AAG GAT GTT TGC AAA AAC TAT GCT (1070)

321                                      330                                        340                               350
glu ala lys asp val phe leu gly met phe leu tyr glu tyr ala arg arg his pro asp tyr ser val val leu leu leu arg leu ala
GAG GCA AAG GAT GTC TTC TTG GGC ATG TTT TTG TAT GAA TAT GCA AGA AGG CAT CCT GAT TAC TCT GTC GTG CTG CTG CTG AGA CTT GCC (1160)

351                                  360 361                                369 370                                   380
lys thr tyr glu thr thr leu glu lys cys cys ala ala ala asp pro his glu cys tyr ala lys val phe asp glu phe lys pro leu
AAG ACA TAT GAA ACC ACT CTA GAG AAG TGC TGT GCC GCT GCA GAT CCT CAT GAA TGC TAT GCC AAA GTG TTC GAT GAA TTT AAA CCT CCT (1250)

381                                  390     392                                400                                   410
val glu glu pro gln asn leu ile lys gln asn cys glu leu phe glu gln leu gly glu tyr lys phe gln asn ala leu leu val arg
GTG GAA GAG CCT CAG AAT TTA ATC AAA CAA AAT TGT GAG CTT TTT GAG CAG CTT GGA GAG TAC AAA TTC CAG AAT GCG CTG TTA GTT CGT (1340)

411                                  420                                    430                           437 438     440
tyr thr lys lys val pro gln val ser thr pro thr leu val glu val ser arg asn leu gly lys val gly ser lys cys cys lys his
TAC ACC AAG AAA GTA CCC CAA GTG TCA ACT CCA ACT CTT GTA GAG GTC TCA AGA AAC CTA GGA AAA GTG GGC AGC AAA TGT TGT AAA CAT (1430)

441                          448     450                                    460 461                                   470
pro glu ala lys arg met pro cys ala glu asp tyr leu ser val val leu asn gln leu cys val leu his glu lys thr pro val ser
CCT GAA GCA AAA AGA ATG CCC TGT GCA GAA GAC TAT CTA TCC GTG GTC CTG AAC CAG TTA TGT GTG TTG CAT GAG AAA ACG CCA GTA AGT (1520)

471                  476 477         480                                    490                                       500
asp arg val thr lys cys cys thr glu ser leu val asn arg arg pro cys phe ser ala leu glu val asp glu thr tyr val pro lys
GAC AGA GTC ACC AAA TGC TGC ACA GAA TCC TTG GTG AAC AGG CGA CCA TGC TTT TCA GCT CTG GAA GTC GAT GAA ACA TAC GTT CCC AAA (1610)

501                                  510             514                    520                                       530
glu phe asn ala glu thr phe thr phe his ala asp ile cys thr leu ser glu lys glu arg gln ile lys lys gln thr ala leu val
GAG TTT AAT GCT GAA ACA TTC ACC TTC CAT GCA GAT ATA TGC ACA CTT TCT GAG AAG GAG AGA CAA ATC AAG AAA CAA ACT GCA CTT GTT (1700)
```

```
531                                    540                                         550                                  558 559 560
glu leu val lys his lys pro lys ala thr lys glu gln leu lys ala val met asp asp phe ala ala phe val glu lys cys cys lys
GAG CTC GTG AAA CAC AAG CCC AAG GCA ACA AAA GAG CAA CTG AAA GCT GTT ATG GAT GAT TTC GCT GCT TTT GTA GAG AAG TGC TGC AAG (1790)

561                         567     570                                            580
ala asp asp lys glu thr cys phe ala glu glu gly lys lys leu val ala ala ser gln ala ala leu gly leu ter             ter
GCT GAC GAT AAG GAG ACC TGC TTT GCC GAG GAG GGT AAA AAA CTT GTT GCT GCA AGT CAA GCT GCC TTA GGC TTA TAA CATCACATTTAAAAG (1883)

                     ter   ter
CATCTCAGCCTACCATGAGAATAAGAGAAAGAAAATGAAGATCAAAAGCTTATTCATCTGTTTTTCTTTTTCGTTGGTGTAAAGCCAACACCCTGTCTAAAAAACATAAATTTCTTTAA (2002)

TCATTTTGCCTCTTTTCTCTGTGCTTCAATTAATAAAAAATGGAAAGAATCTAA..... 20 .....AA (2078)
```

9. Nucleotide sequence coding for the pre pro human serum albumin, said nucleotide sequence is as follows:

```
                                                            -18         p   r   o           -10
                                                            Met lys trp val tlu phe ile ser leu leu phe leu phe ser
                                                            ATG AAG TGG GTA ACC TTT ATT TCC CTT CTT TTT CTC TTT AGC  (30)

            -1  -6      p   r   o       -1   1                                  10                                      20
ser ala tyr ser arg gly val phe arg arg asp ala his lys ser glu val ala his arg phe lys asp leu gly glu glu asn phe lys
TCG GCT TAT TCC AGG GGT GTG TTT CGT CGA GAT GCA CAC AAG AGT GAG GTT GCT CAT CGG TTT AAA GAT TTG GGA GAA GAA AAT TTC AAA (170)

21                                      30          34                          40                                      50
ala leu val leu ile ala phe ala gln tyr leu gln gln cys pro phe glu asp his val lys leu val asn glu val thr glu phe ala
GCC TTG GTG TTG ATT GCC TTT GCT CAG TAT CTT CAG CAG TGT CCA TTT GAA GAT CAT GTA AAA TTA GTG AAT GAA GTA ACT GAA TTT GCA (260)

51      53                              60      62                              70                  75                  80
lys thr cys val ala asp glu ser ala glu asn cys asp lys ser leu his thr leu phe gly asp lys leu cys thr val ala thr leu
AAA ACA TGT GTT GCT GAT GAG TCA GCT GAA AAT TGT GAC AAA TCA CTT CAT ACC CTT TTT GGA GAC AAA TTA TGC ACA GTT GCA ACT CTT (350)

81                                      90  91                                  100 101                                 110
arg glu thr tyr gly glu met ala asp cys cys ala lys gln glu pro gly arg asn glu cys phe leu gln his lys asp asp asn pro
CGT GAA ACC TAT GGT GAA ATG GCT GAC TGC TGT GCA AAA CAA GAA CCT GGG AGA AAT GAA TGC TTC TTG CAA CAC AAA GAT GAC AAC CCA (440)

111                                     120         124                         130                                     140
asn leu pro arg leu val arg pro glu val asp val met cys thr ala phe his asp asn glu glu thr phe leu lys lys tyr leu try
AAC CTC CCC CGA TTG GTG AGA CCA GAG GTT GAT GTG ATG TGC ACT GCT TTT CAT GAC AAT GAA GAG ACA TTT TTG AAA AAA TAC TTA TAT (330)

141                                     150                                     160                             168 169 170
glu ile ala arg arg his pro tyr phe tyr ala pro glu leu leu phe phe ala lys arg tyr lys ala ala phe thr glu cys cys gln
GAA ATT GCC AGA AGA CAT CCT TAC TTT TAT GCC CCG GAA CTC CTT TTC TTT GCT AAA AGG TAT AAA GCT GCT TTT ACA GAA TGT TGC CAA (620)

171                         177         180                                     190                                     200
ala ala asp lys ala ala cys leu leu pro lys leu asp glu leu arg asp glu gly lys ala ser ser ala lys gln arg leu lys cys
GCT GCT GAT AAA GCT GCC TGC CTG TTG CCA AAG CTC GAT GAA CTT CGG GAT GAA GGG AAG GCT TCG TCT GCC AAA CAG AGA CTC AAG TGT (710)

201                                     210                                     220                                     230
ala ser leu gln lys phe gly glu arg ala phe lys ala trp ala val ala arg leu ser gln arg phe pro lys ala glu phe ala glu
GCC AGT CTC CAA AAA TTT GGA GAA AGA GCT TTC AAA GCA TGG GCA GTA GCT CGC CTG AGC CAG AGA TTT CCC AAA GCT GAG TTT GCA GAA (300)
```

231									240					245	246				250			253							260	
val	ser	lys	leu	val	thr	asp	leu	thr	lys	val	his	thr	glu	cys	cys	his	gly	asp	leu	leu	glu	cys	ala	asp	asp	arg	ala	asp	leu	
GTT	TCC	AAG	TTA	GTG	ACA	GAT	CTT	ACC	AAA	GTC	CAC	ACG	GAA	TGC	TGC	CAT	GGA	GAT	CTG	CTT	GAA	TGT	GCT	GAT	GAC	AGG	GCG	GAC	CTT	(890)
261				265					270								278	279	280									289	290	
ala	lys	tyr	ile	cys	glu	asn	gln	asp	ser	ile	ser	ser	lys	leu	lys	glu	cys	cys	glu	lys	pro	leu	leu	glu	lys	ser	his	cys	ile	
GCC	AAG	TAT	ATC	TGT	GAA	AAT	CAA	GAT	TCG	ATC	TCC	AGT	AAA	CTG	AAG	GAA	TGC	TGT	GAA	AAA	CCT	CTG	TTG	GAA	AAA	TCC	CAC	TGC	ATT	(980)
291									300										310						316				320	
ala	glu	val	glu	asn	asp	glu	met	pro	ala	asp	leu	pro	ser	leu	ala	ala	asp	phe	val	glu	ser	lys	asp	val	cys	lys	asn	tyr	ala	
GCC	GAA	GTG	GAA	AAT	GAT	GAG	ATG	CCT	GCT	GAC	TTG	CCT	TCA	TTA	GCT	GCT	GAT	TTT	GTT	GAA	AGT	AAG	GAT	GTT	TGC	AAA	AAC	TAT	GCT	(1070)
321									330										340										350	
glu	ala	lys	asp	val	phe	leu	gly	met	phe	leu	tyr	glu	tyr	ala	arg	arg	his	pro	asp	tyr	ser	val	val	leu	leu	leu	arg	leu	ala	
GAG	GCA	AAG	GAT	GTC	TTC	TTG	GGC	ATG	TTT	TTG	TAT	GAA	TAT	GCA	AGA	AGG	CAT	CCT	GAT	TAC	TCT	GTC	GTG	CTG	CTG	CTG	AGA	CTT	GCC	(1160)
351									360	361								369	370										380	
lys	thr	tyr	glu	thr	thr	leu	glu	lys	cys	cys	ala	ala	ala	asp	pro	his	glu	cys	tyr	ala	lys	val	phe	asp	glu	phe	lys	pro	leu	
AAG	ACA	TAT	GAA	ACC	ACT	CTA	GAG	AAG	TGC	TGT	GCC	GCT	GCA	GAT	CCT	CAT	GAA	TGC	TAT	GCC	AAA	GTG	TTC	GAT	GAA	TTT	AAA	CCT	CTT	(1250)
381									390		392								400										410	
val	glu	glu	pro	gln	asn	leu	ile	lys	gln	asn	cys	glu	leu	phe	glu	gln	leu	gly	glu	tyr	lys	phe	gln	asn	ala	leu	leu	val	arg	
GTG	GAA	GAG	CCT	CAG	AAT	TTA	ATC	AAA	CAA	AAT	TGT	GAG	CTT	TTT	GAG	CAG	CTT	GGA	GAG	TAC	AAA	TTC	CAG	AAT	GCG	CTG	TTA	GTT	CGT	(1340)
411									420										430							437	438		440	
tyr	thr	lys	lys	val	pro	gln	val	ser	thr	pro	thr	leu	val	glu	val	ser	arg	asn	leu	gly	lys	val	gly	ser	lys	cys	cys	lys	his	
TAC	ACC	AAG	AAA	GTA	CCC	CAA	GTG	TCA	ACT	CCA	ACT	CTT	GTA	GAG	GTC	TCA	AGA	AAC	CTA	GGA	AAA	GTG	GGC	AGC	AAA	TGT	TGT	AAA	CAT	(1430)
441							448		450										460	461									470	
pro	glu	ala	lys	arg	met	pro	cys	ala	glu	asp	tyr	leu	ser	val	val	leu	asn	gln	leu	cys	val	leu	his	glu	lys	thr	pro	val	ser	
CCT	GAA	GCA	AAA	AGA	ATG	CCC	TGT	GCA	GAA	GAC	TAT	CTA	TCC	GTG	GTC	CTG	AAC	CAG	TTA	TGT	GTG	TTG	CAT	GAG	AAA	ACG	CCA	GTA	AGT	(1520)
471					476	477			480										490										500	
asp	arg	val	thr	lys	cys	cys	thr	glu	ser	leu	val	asn	arg	arg	pro	cys	phe	ser	ala	leu	glu	val	asp	glu	thr	tyr	val	pro	lys	
GAC	AGA	GTC	ACC	AAA	TGC	TGC	ACA	GAA	TCC	TTG	GTG	AAC	AGG	CGA	CCA	TGC	TTT	TCA	GCT	CTG	GAA	GTC	GAT	GAA	ACA	TAC	GTT	CCC	AAA	(1610)
501									510				514						520										530	
glu	phe	asn	ala	glu	thr	phe	thr	phe	his	ala	asp	ile	cys	thr	leu	ser	glu	lys	glu	arg	gln	ile	lys	lys	gln	thr	ala	leu	val	
GAG	TTT	AAT	GCT	GAA	ACA	TTC	ACC	TTC	CAT	GCA	GAT	ATA	TGC	ACA	CTT	TCT	GAG	AAG	GAG	AGA	CAA	ATC	AAG	AAA	CAA	ACT	GCA	CTT	GTT	(1700)

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                                                                    540
531                                                                 550                                                 558 559 560
glu leu val lys his lys pro lys ala thr lys glu gln leu lys ala val met asp asp phe ala ala phe val glu lys cys cys lys
CAG CTC GTG AAA CAC AAG CCC AAG GCA ACA AAA GAG CAA CTG AAA GCT GTT ATG GAT GAT TTC GCT TTT GTA GAG AAG TGC TGC AAG (1790)

                                                                    570
561                                                                 580
ala asp asp lys glu thr cys phe ala glu glu gly lys lys leu val ala ala ser gln ala ala leu gly leu ter          ter
GCT GAC GAT AAG GAG ACC TGC TTT GCC GAG GGT AAA AAA CTT GTT GCT GCA AGT CAA GCT GCC TTA GGC TTA TAA CATCACATTTAAAAG (1883)

                                                                                                                ter   ter
CATCTCAGCCTACCATGAGAATAAGAGAAAGAAATGAAGATCAAAAGCTTATTCATCTGTTTTTTCTTTTTTCGTTGCTGTAAAGCCAACACCCTGTCTAAAAAAACATAAATTTTCTTTAA (2002)

TCATTTTGCCTCTTTTCTCTGTGCTTCAATTAATAAAAAATGGAAAGAATCTAA..... 20 .....AA (2078)
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10. A nucleotide sequence according to any of claims 6 to 9, in essentially pure form.

11. A DNA transfer vector comprising a nucleotide sequence as defined in claim 5.

12. A DNA transfer vector according to claim 11, transferred to and replicated in a micro-organism.

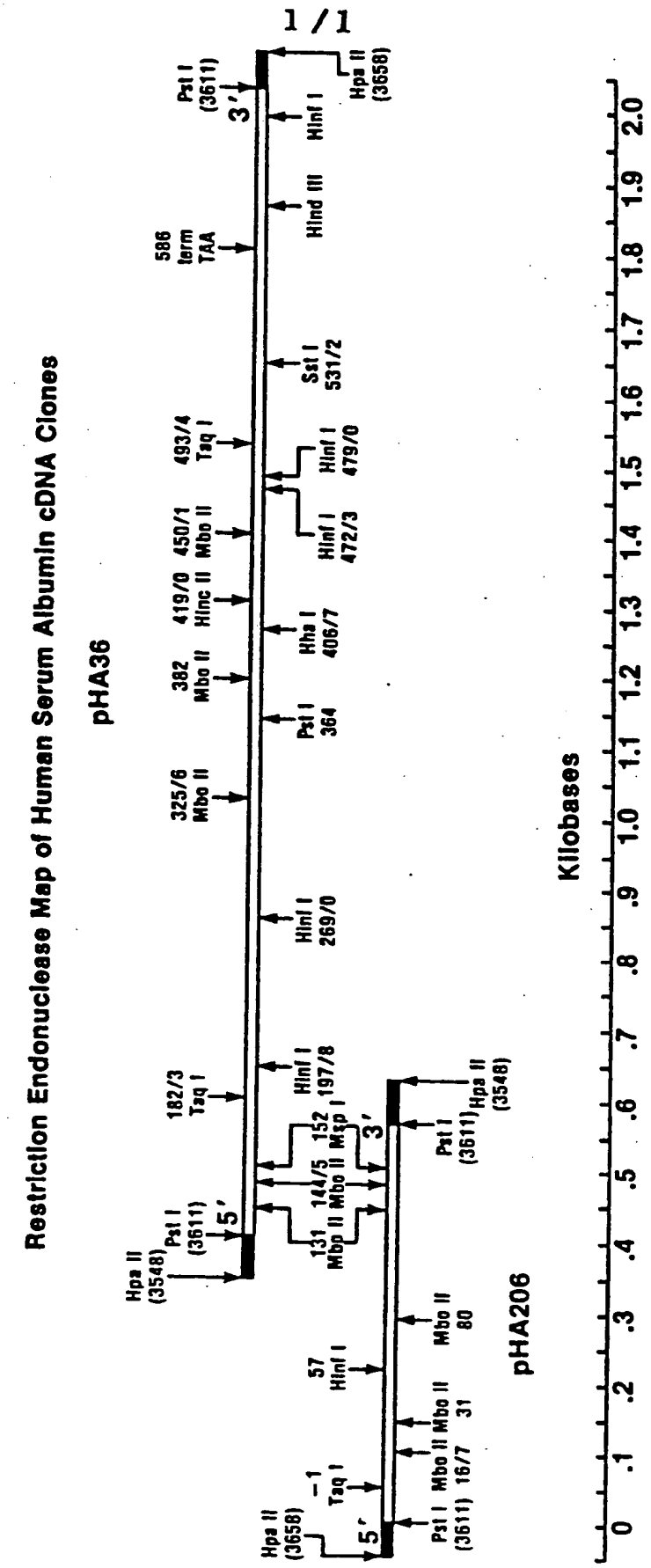
13. A DNA transfer vector according to claim 12, which is a plasmid.

14. A DNA transfer vector according to claim 13, wherein the plasmid is pBR322 or YEp6.

15. A process for preparing human serum albumin, which comprises culturing a micro-organism according to claim 5.

16. A DNA transfer vector according to any of claims 12 to 14, or a process according to claim 15, wherein the micro-organism is a bacterium or yeast.

17. A vector or process according to claim 16, wherein the bacterium or yeast is E. coli or Saccharomyces cerevisiae.


Restriction Endonuclease Map of Human Serum Albumin cDNA Clones
pHA36
pHA206
Kilobases
0
.1
.2
.3
.4
.5
.6
.7
.8
.9
1.0
1.1
1.2
1.3
1.4
1.5
1.6
1.7
1.8
1.9
2.0
Hpa II (3548)
Pst I (3611)
5'
182/3 Taq I
325/6 Mbo II
382 Mbo II
419/0 Hinc II
450/1 Mbo II
493/4 Taq I
586 term TAA
Pst I (3611)
3'
Hpa II (3658)
Hinf I 269/0
Pst I 364
Hha I 406/7
Hinf I 472/3
Hinf I 479/0
Sst I 531/2
Hind III
Hinf I
Hinf I 197/8
131 Mbp II
144/5 Mbo II
152 Msp I
3'
Pst I (3611)
Hpa II (3548)
Hpa II (3658)
-1
Taq I
5'
57 Hinf I
Mbo II 80
Pst I (3611)
Mbo II 16/7
Mbo II 31